

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Johnson, Gary L.
- (ii) TITLE OF INVENTION: Method and Product for Regulating Apoptosis
- (iii) NUMBER OF SEQUENCES: 12
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: LAHIVE & COCKFIELD
 - (B) STREET: 28 State Street
 - (C) CITY: Boston
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02109
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: ASCII(text)
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/039,740
 - (B) FILING DATE: 14-FEB-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Kara, Catherine J.
 - (B) REGISTRATION NUMBER: 41,106
 - (C) REFERENCE/DOCKET NUMBER: CPI-042
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (617) 227-7400
 - (B) TELEFAX: (617) 742-4214

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 3260 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 486..2501
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TACACTCCTT GCCACAGTCT GGCAGAAAGA ATCAAACCTC AGAGACTCCT CCGGCCAGTT

GTAGACACTA TCCTTGTCAG GTGTGCAGAT CCAACAGCCG CACGAGTCAG CTGTCCATAT	120
CTACAGTGCT GGAACCTCTGC AAGGGCCAAG CAGGAGAGCT GGCGGTTGGG AGAGAAATAC	180
TTAAAGCTGG GTCCATCGGG GTTGGTGGTG TCGATTACGT CTTAAGTTGT ATCCTTGGA	240
ACCAAGCTGA ATCAAACAAC TGGCAAGAAC TGCTGGGTCG CCTCTGTCTT ATAGACAGGT	300
TGCTGTTGGA ATTTCTGCT GAATTCTATC CTCATATTGT CAGTACTGAT GTCTCACAAG	360
CTGAGCCTGT TGAAATCAGG TACAAGAAGC TGCTCTCCCT CTTAACCTTT GCCTTGCAAT	420
CCATTGACAA TTCCCACTCG ATGGTTGGCA AGCTCTCTCG GAGGATATAT CTGAGCTCTG	480
CCAGG ATG GTG ACC GCA GTG CCC GCT GTG TTT TCC AAG CTG GTA ACC	527
Met Val Thr Ala Val Pro Ala Val Phe Ser Lys Leu Val Thr	
1 5 10	
ATG CTT AAT GCT TCT GGC TCC ACC CAC TTC ACC AGG ATG CGC CGG CGT	575
Met Leu Asn Ala Ser Gly Ser Thr His Phe Thr Arg Met Arg Arg Arg	
15 20 25 30	
CTG ATG GCT ATC GCG GAT GAG GTA GAA ATT GCC GAG GTC ATC CAG CTG	623
Leu Met Ala Ile Ala Asp Glu Val Glu Ile Ala Glu Val Ile Gln Leu	
35 40 45	
GGT GTG GAG GAC ACT GTG GAT GGG CAT CAG GAC AGC TTA CAG GCC GTG	671
Gly Val Glu Asp Thr Val Asp Gly His Gln Asp Ser Leu Gln Ala Val	
50 55 60	
GCC CCC ACC AGC TGT CTA GAA AAC AGC TCC CTT GAG CAC ACA GTC CAT	719
Ala Pro Thr Ser Cys Leu Glu Asn Ser Ser Leu Glu His Thr Val His	
65 70 75	
AGA GAG AAA ACT GGA AAA GGA CTA AGT GCT ACG AGA CTG AGT GCC AGC	767
Arg Glu Lys Thr Gly Lys Gly Leu Ser Ala Thr Arg Leu Ser Ala Ser	
80 85 90	
TCG GAG GAC ATT TCT GAC AGA CTG GCC GGC GTC TCT GTA GGA CTT CCC	815
Ser Glu Asp Ile Ser Asp Arg Leu Ala Gly Val Ser Val Gly Leu Pro	
95 100 105 110	
AGC TCA ACA ACA ACA GAA CAA CCA AAG CCA GCG GTT CAA ACA AAA GGC	863
Ser Ser Thr Thr Thr Glu Gln Pro Lys Pro Ala Val Gln Thr Lys Gly	
115 120 125	
AGA CCC CAC AGT CAG TGT TTG AAC TCC TCC CCT TTG TCT CAT GCT CAA	911
Arg Pro His Ser Gln Cys Leu Asn Ser Ser Pro Leu Ser His Ala Gln	
130 135 140	
TTA ATG TTC CCA GCA CCA TCA GCC CCT TGT TCC TCT GCC CCG TCT GTC	959
Leu Met Phe Pro Ala Pro Ser Ala Pro Cys Ser Ser Ala Pro Ser Val	
145 150 155	
CCA GAT ATT TCT AAG CAC AGA CCC CAG GCA TTT GTT CCC TGC AAA ATA	1007

Pro	Asp	Ile	Ser	Lys	His	Arg	Pro	Gln	Ala	Phe	Val	Pro	Cys	Lys	Ile	
160						165					170					
CCT	TCC	GCA	TCT	CCT	CAG	ACA	CAG	CGC	AAG	TTC	TCT	CTA	CAA	TTC	CAG	1055
Pro	Ser	Ala	Ser	Pro	Gln	Thr	Gln	Arg	Lys	Phe	Ser	Leu	Gln	Phe	Gln	
175					180					185					190	
AGG	AAC	TGC	TCT	GAA	CAC	CGA	GAC	TCA	GAC	CAG	CTC	TCC	CCA	GTC	TTC	1103
Arg	Asn	Cys	Ser	Glu	His	Arg	Asp	Ser	Asp	Gln	Leu	Ser	Pro	Val	Phe	
				195					200					205		
ACT	CAG	TCA	AGA	CCC	CCA	CCC	TCC	AGT	AAC	ATA	CAC	AGG	CCA	AAG	CCA	1151
Thr	Gln	Ser	Arg	Pro	Pro	Pro	Ser	Ser	Asn	Ile	His	Arg	Pro	Lys	Pro	
			210					215					220			
TCC	CGA	CCC	GTT	CCG	GGC	AGT	ACA	AGC	AAA	CTA	GGG	GAC	GCC	ACA	AAA	1199
Ser	Arg	Pro	Val	Pro	Gly	Ser	Thr	Ser	Lys	Leu	Gly	Asp	Ala	Thr	Lys	
		225					230					235				
AGT	AGC	ATG	ACA	CTT	GAT	CTG	GGC	AGT	GCT	TCC	AGG	TGT	GAC	GAC	AGC	1247
Ser	Ser	Met	Thr	Leu	Asp	Leu	Gly	Ser	Ala	Ser	Arg	Cys	Asp	Asp	Ser	
	240					245					250					
TTT	GGC	GGC	GGC	GGC	AAC	AGT	GGC	AAC	GCC	GTC	ATA	CCC	AGC	GAC	GAG	1295
Phe	Gly	Gly	Gly	Gly	Asn	Ser	Gly	Asn	Ala	Val	Ile	Pro	Ser	Asp	Glu	
255					260					265					270	
ACA	GTG	TTC	ACG	CCG	GTG	GAG	GAC	AAG	TGC	AGG	TTA	GAT	GTG	AAC	ACC	1343
Thr	Val	Phe	Thr	Pro	Val	Glu	Asp	Lys	Cys	Arg	Leu	Asp	Val	Asn	Thr	
				275					280					285		
GAG	CTC	AAC	TCC	AGC	ATC	GAG	GAC	CTT	CTT	GAA	GCA	TCC	ATG	CCT	TCA	1391
Glu	Leu	Asn	Ser	Ser	Ile	Glu	Asp	Leu	Leu	Glu	Ala	Ser	Met	Pro	Ser	
			290					295					300			
AGT	GAC	ACG	ACA	GTC	ACT	TTC	AAG	TCC	GAA	GTC	GCC	GTC	CTC	TCT	CCG	1439
Ser	Asp	Thr	Thr	Val	Thr	Phe	Lys	Ser	Glu	Val	Ala	Val	Leu	Ser	Pro	
		305					310					315				
GAA	AAG	GCC	GAA	AAT	GAC	GAC	ACC	TAC	AAA	GAC	GAC	GTC	AAT	CAT	AAT	1487
Glu	Lys	Ala	Glu	Asn	Asp	Asp	Thr	Tyr	Lys	Asp	Asp	Val	Asn	His	Asn	
	320					325					330					
CAA	AAG	TGC	AAA	GAA	AAG	ATG	GAA	GCT	GAA	GAG	GAG	GAG	GCT	TTA	GCG	1535
Gln	Lys	Cys	Lys	Glu	Lys	Met	Glu	Ala	Glu	Glu	Glu	Glu	Ala	Leu	Ala	
335					340					345					350	
ATC	GCC	ATG	GCG	ATG	TCA	GCG	TCT	CAG	GAT	GCC	CTC	CCC	ATC	GTC	CCT	1583
Ile	Ala	Met	Ala	Met	Ser	Ala	Ser	Gln	Asp	Ala	Leu	Pro	Ile	Val	Pro	
				355					360					365		
CAG	CTG	CAG	GTG	GAA	AAT	GGA	GAA	GAT	ATT	ATC	ATC	ATT	CAG	CAG	GAC	1631
Gln	Leu	Gln	Val	Glu	Asn	Gly	Glu	Asp	Ile	Ile	Ile	Ile	Gln	Gln	Asp	
			370					375					380			
ACA	CCA	GAA	ACT	CTT	CCA	GGA	CAT	ACC	AAA	GCG	AAA	CAG	CCT	TAC	AGA	1679

Thr	Pro	Glu	Thr	Leu	Pro	Gly	His	Thr	Lys	Ala	Lys	Gln	Pro	Tyr	Arg	
	385						390					395				
GAA	GAC	GCT	GAG	TGG	CTG	AAA	GGC	CAG	CAG	ATA	GGC	CTC	GGA	GCA	TTT	1727
Glu	Asp	Ala	Glu	Trp	Leu	Lys	Gly	Gln	Gln	Ile	Gly	Leu	Gly	Ala	Phe	
	400					405					410					
TCT	TCC	TGT	TAC	CAA	GCA	CAG	GAT	GTG	GGG	ACT	GGG	ACT	TTA	ATG	GCT	1775
Ser	Ser	Cys	Tyr	Gln	Ala	Gln	Asp	Val	Gly	Thr	Gly	Thr	Leu	Met	Ala	
415					420				425						430	
GTG	AAA	CAG	GTG	ACG	TAC	GTC	AGA	AAC	ACA	TCC	TCC	GAG	CAG	GAG	GAG	1823
Val	Lys	Gln	Val	Thr	Tyr	Val	Arg	Asn	Thr	Ser	Ser	Glu	Gln	Glu	Glu	
				435					440					445		
GTG	GTG	GAA	GCG	TTG	AGG	GAA	GAG	ATC	CGG	ATG	ATG	GGT	CAC	CTC	AAC	1871
Val	Val	Glu	Ala	Leu	Arg	Glu	Glu	Ile	Arg	Met	Met	Gly	His	Leu	Asn	
			450					455					460			
CAT	CCA	AAC	ATC	ATC	CGG	ATG	CTG	GGG	GCC	ACG	TGC	GAG	AAG	AGC	AAC	1919
His	Pro	Asn	Ile	Ile	Arg	Met	Leu	Gly	Ala	Thr	Cys	Glu	Lys	Ser	Asn	
		465					470					475				
TAC	AAC	CTC	TTC	ATT	GAG	TGG	ATG	GCG	GGA	GGA	TCT	GTG	GCT	CAC	CTC	1967
Tyr	Asn	Leu	Phe	Ile	Glu	Trp	Met	Ala	Gly	Gly	Ser	Val	Ala	His	Leu	
	480					485					490					
TTG	AGT	AAA	TAC	GGA	GCT	TTC	AAG	GAG	TCA	GTC	GTC	ATT	AAC	TAC	ACT	2015
Leu	Ser	Lys	Tyr	Gly	Ala	Phe	Lys	Glu	Ser	Val	Val	Ile	Asn	Tyr	Thr	
495					500					505					510	
GAG	CAG	TTA	CTG	CGT	GGC	CTT	TCC	TAT	CTC	CAC	GAG	AAC	CAG	ATC	ATT	2063
Glu	Gln	Leu	Leu	Arg	Gly	Leu	Ser	Tyr	Leu	His	Glu	Asn	Gln	Ile	Ile	
				515					520					525		
CAC	AGA	GAC	GTC	AAA	GGT	GCC	AAC	CTG	CTC	ATT	GAC	AGC	ACC	GGT	CAG	2111
His	Arg	Asp	Val	Lys	Gly	Ala	Asn	Leu	Leu	Ile	Asp	Ser	Thr	Gly	Gln	
			530					535					540			
AGG	CTG	AGA	ATT	GCA	GAC	TTT	GGA	GCT	GCT	GCC	AGG	TTG	GCA	TCA	AAA	2159
Arg	Leu	Arg	Ile	Ala	Asp	Phe	Gly	Ala	Ala	Ala	Arg	Leu	Ala	Ser	Lys	
		545					550					555				
GGA	ACC	GGT	GCA	GGA	GAG	TTC	CAG	GGA	CAG	TTA	CTG	GGG	ACA	ATT	GCA	2207
Gly	Thr	Gly	Ala	Gly	Glu	Phe	Gln	Gly	Gln	Leu	Leu	Gly	Thr	Ile	Ala	
		560				565					570					
TTC	ATG	GCG	CCT	GAG	GTC	CTA	AGA	GGT	CAG	CAG	TAT	GGT	AGG	AGC	TGT	2255
Phe	Met	Ala	Pro	Glu	Val	Leu	Arg	Gly	Gln	Gln	Tyr	Gly	Arg	Ser	Cys	
575					580					585					590	
GAT	GTA	TGG	AGT	GTT	GGC	TGC	GCC	ATT	ATA	GAA	ATG	GCT	TGT	GCA	AAA	2303
Asp	Val	Trp	Ser	Val	Gly	Cys	Ala	Ile	Ile	Glu	Met	Ala	Cys	Ala	Lys	
				595					600					605		
CCA	CCT	TGG	AAT	GCA	GAA	AAA	CAC	TCC	AAT	CAT	CTC	GCC	TTG	ATA	TTT	2351

Pro	Pro	Trp	Asn	Ala	Glu	Lys	His	Ser	Asn	His	Leu	Ala	Leu	Ile	Phe	
			610					615					620			
AAG	ATT	GCT	AGC	GCA	ACT	ACT	GCA	CCG	TCC	ATC	CCG	TCA	CAC	CTG	TCC	2399
Lys	Ile	Ala	Ser	Ala	Thr	Thr	Ala	Pro	Ser	Ile	Pro	Ser	His	Leu	Ser	
		625					630				635					
CCG	GGT	CTG	CGC	GAC	GTG	GCC	GTG	CGC	TGC	TTA	GAA	CTT	CAG	CCT	CAG	2447
Pro	Gly	Leu	Arg	Asp	Val	Ala	Val	Arg	Cys	Leu	Glu	Leu	Gln	Pro	Gln	
	640					645				650						
GAC	CGG	CCT	CCG	TCC	AGA	GAG	CTG	CTG	AAA	CAT	CCG	GTC	TTC	CGT	ACC	2495
Asp	Arg	Pro	Pro	Ser	Arg	Glu	Leu	Leu	Lys	His	Pro	Val	Phe	Arg	Thr	
655				660				665			670					
ACG	TGG	TAGTTAATTG	TTCAGATCAG	CTCTAATGGA	GACAGGATAT	CGAACCGGGA										2551
Thr	Trp															
GAGAGAAAAG	AGAACTTG	GGCGACCATG	CCGCTAACCG	CAGCCCTCAC	GCCACTGAAC											2611
AGCCAGAAAC	GGGGCCAGCG	GGGAACCGTA	CCTAAGCATG	TGATTGACAA	ATCATGACCT											2671
GTACCTAAGC	TCGATATGCA	GACATCTACA	GCTCGTGCAG	GAAGTGCACA	CCGTGCCTTT											2731
CACAGGACTG	GCTCTGGGGG	ACCAGGAAGG	CGATGGAGTT	TGCATGACTA	AAGAACAGAA											2791
GCATAAATTT	ATTTTTGGAG	CACTTTTTTCA	GCTAATCAGT	ATTACCATGT	ACATCAACAT											2851
GCCCGCCACA	TTTCAAATC	AGACTGTCCC	AGATGTCAAG	ATCCACTGTG	TTTGAGTTTG											2911
TTTGCAATTC	CCTCAGCTTG	CTGGTAATTG	TGGTGTGTTTG	TTTTCGATGC	AAATGTGATG											2971
TAATATTCTT	ATTTTCTTTG	GATCAAAGCT	GGACTGAAAA	TTGTACTGTG	TAATTATTTT											3031
TGTGTTTTTA	ATGTTATTTG	GTAATCGAAT	TGTAAATAAC	GTCTACTGCT	GTTTATTCCA											3091
GTTTCTACTA	CCTCAGGTGT	CCTATAGATT	TTTCTTCTAC	CAAAGTTCAC	TCTCAGAATG											3151
AAATTCTACG	TGCTGTGTGA	CTATGACTCC	TAAGACTTCC	AGGGCTTAAG	GGCTAACTCC											3211
TATTAGCACC	TTACTATGTA	AGCAAATGCT	ACAAAAAAAA	AAAAAAAA												3260

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 672 AA
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Val	Thr	Ala	Val	Pro	Ala	Val	Phe	Ser	Lys	Leu	Val	Thr	Met	Leu
1				5					10					15	

Asn	Ala	Ser	Gly	Ser	Thr	His	Phe	Thr	Arg	Met	Arg	Arg	Arg	Leu	Met	20	25	30
Ala	Ile	Ala	Asp	Glu	Val	Glu	Ile	Ala	Glu	Val	Ile	Gln	Leu	Gly	Val	35	40	45
Glu	Asp	Thr	Val	Asp	Gly	His	Gln	Asp	Ser	Leu	Gln	Ala	Val	Ala	Pro	50	55	60
Thr	Ser	Cys	Leu	Glu	Asn	Ser	Ser	Leu	Glu	His	Thr	Val	His	Arg	Glu	65	70	75
Lys	Thr	Gly	Lys	Gly	Leu	Ser	Ala	Thr	Arg	Leu	Ser	Ala	Ser	Ser	Glu	85	90	95
Asp	Ile	Ser	Asp	Arg	Leu	Ala	Gly	Val	Ser	Val	Gly	Leu	Pro	Ser	Ser	100	105	110
Thr	Thr	Thr	Glu	Gln	Pro	Lys	Pro	Ala	Val	Gln	Thr	Lys	Gly	Arg	Pro	115	120	125
His	Ser	Gln	Cys	Leu	Asn	Ser	Ser	Pro	Leu	Ser	His	Ala	Gln	Leu	Met	130	135	140
Phe	Pro	Ala	Pro	Ser	Ala	Pro	Cys	Ser	Ser	Ala	Pro	Ser	Val	Pro	Asp	145	150	155
Ile	Ser	Lys	His	Arg	Pro	Gln	Ala	Phe	Val	Pro	Cys	Lys	Ile	Pro	Ser	165	170	175
Ala	Ser	Pro	Gln	Thr	Gln	Arg	Lys	Phe	Ser	Leu	Gln	Phe	Gln	Arg	Asn	180	185	190
Cys	Ser	Glu	His	Arg	Asp	Ser	Asp	Gln	Leu	Ser	Pro	Val	Phe	Thr	Gln	195	200	205
Ser	Arg	Pro	Pro	Pro	Ser	Ser	Asn	Ile	His	Arg	Pro	Lys	Pro	Ser	Arg	210	215	220
Pro	Val	Pro	Gly	Ser	Thr	Ser	Lys	Leu	Gly	Asp	Ala	Thr	Lys	Ser	Ser	225	230	235
Met	Thr	Leu	Asp	Leu	Gly	Ser	Ala	Ser	Arg	Cys	Asp	Asp	Ser	Phe	Gly	245	250	255
Gly	Gly	Gly	Asn	Ser	Gly	Asn	Ala	Val	Ile	Pro	Ser	Asp	Glu	Thr	Val	260	265	270
Phe	Thr	Pro	Val	Glu	Asp	Lys	Cys	Arg	Leu	Asp	Val	Asn	Thr	Glu	Leu	275	280	285
Asn	Ser	Ser	Ile	Glu	Asp	Leu	Leu	Glu	Ala	Ser	Met	Pro	Ser	Ser	Asp	290	295	300
Thr	Thr	Val	Thr	Phe	Lys	Ser	Glu	Val	Ala	Val	Leu	Ser	Pro	Glu	Lys			

305		310		315		320
Ala Glu Asn Asp Asp Thr Tyr Lys Asp Asp Val Asn His Asn Gln Lys						
		325		330		335
Cys Lys Glu Lys Met Glu Ala Glu Glu Glu Glu Ala Leu Ala Ile Ala		340		345		350
Met Ala Met Ser Ala Ser Gln Asp Ala Leu Pro Ile Val Pro Gln Leu		355		360		365
Gln Val Glu Asn Gly Glu Asp Ile Ile Ile Ile Gln Gln Asp Thr Pro		370		375		380
Glu Thr Leu Pro Gly His Thr Lys Ala Lys Gln Pro Tyr Arg Glu Asp		385		390		400
Ala Glu Trp Leu Lys Gly Gln Gln Ile Gly Leu Gly Ala Phe Ser Ser		405		410		415
Cys Tyr Gln Ala Gln Asp Val Gly Thr Gly Thr Leu Met Ala Val Lys		420		425		430
Gln Val Thr Tyr Val Arg Asn Thr Ser Ser Glu Gln Glu Glu Val Val		435		440		445
Glu Ala Leu Arg Glu Glu Ile Arg Met Met Gly His Leu Asn His Pro		450		455		460
Asn Ile Ile Arg Met Leu Gly Ala Thr Cys Glu Lys Ser Asn Tyr Asn		465		470		480
Leu Phe Ile Glu Trp Met Ala Gly Gly Ser Val Ala His Leu Leu Ser		485		490		495
Lys Tyr Gly Ala Phe Lys Glu Ser Val Val Ile Asn Tyr Thr Glu Gln		500		505		510
Leu Leu Arg Gly Leu Ser Tyr Leu His Glu Asn Gln Ile Ile His Arg		515		520		525
Asp Val Lys Gly Ala Asn Leu Leu Ile Asp Ser Thr Gly Gln Arg Leu		530		535		540
Arg Ile Ala Asp Phe Gly Ala Ala Ala Arg Leu Ala Ser Lys Gly Thr		545		550		555
Gly Ala Gly Glu Phe Gln Gly Gln Leu Leu Gly Thr Ile Ala Phe Met		565		570		575
Ala Pro Glu Val Leu Arg Gly Gln Gln Tyr Gly Arg Ser Cys Asp Val		580		585		590
Trp Ser Val Gly Cys Ala Ile Ile Glu Met Ala Cys Ala Lys Pro Pro		595		600		605

Trp Asn Ala Glu Lys His Ser Asn His Leu Ala Leu Ile Phe Lys Ile
 610 615 620

Ala Ser Ala Thr Thr Ala Pro Ser Ile Pro Ser His Leu Ser Pro Gly
 625 630 635 640

Leu Arg Asp Val Ala Val Arg Cys Leu Glu Leu Gln Pro Gln Asp Arg
 645 650 655

Pro Pro Ser Arg Glu Leu Leu Lys His Pro Val Phe Arg Thr Thr Trp
 660 665 670

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1493 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Ala Ala Ala Ala Gly Asp Arg Ala Ser Ser
 Ser Gly Phe Pro Gly Ala Ala Ala Ala Ser Pro Glu Ala Gly Gly Gly
 Gly Gly Gly Gly Gly Ala Leu Gln Gly Ser Gly Ala Pro Ala Ala Gly
 Ala Ala Gly Leu Leu Arg Glu Pro Gly Ser Ala Gly Arg Glu Arg Ala Asp
 Trp Arg Arg Arg Gln Leu Arg Lys Val Arg Ser Val Glu Leu Asp Gln
 Leu Pro Glu Gln Pro Leu Phe Leu Ala Ala Ala Ser Pro Pro Cys Pro Ser
 Thr Ser Pro Ser Pro Glu Pro Ala Asp Ala Ala Ala Gly Ala Ser Arg Phe Gln
 Pro Ala Ala Gly Pro Pro Pro Pro Gly Ala Ala Ser Arg
 Cys Gly Ser His Ser Ala Glu Leu Ala Ala Ala Arg Asp Ser Gly Ala
 Arg Ser Pro Ala Gly Ala Glu Pro Pro Ser Ala Ala Ala Pro Ser Gly
 Arg Glu Met Glu Asn Lys Glu Thr Leu Lys Gly Leu His Lys Met Glu
 Asp Arg Pro Glu Glu Arg Met Ile Arg Glu Lys Leu Lys Ala Thr Cys
 Met Pro Ala Trp Lys His Glu Trp Leu Glu Arg Arg Asn Arg Arg Gly
 Pro Val Val Val Lys Pro Ile Pro Ile Lys Gly Asp Gly Ser Glu Val
 Asn Asn Leu Ala Ala Glu Pro Gln Gly Glu Gly Gln Ala Gly Ser Ala
 Ala Pro Ala Pro Lys Gly Arg Arg Ser Pro Ser Pro Gly Ser Ser Pro
 Ser Gly Arg Ser Val Lys Pro Glu Ser Pro Gly Val Arg Arg Lys Arg
 Val Ser Pro Val Pro Phe Gln Ser Gly Arg Ile Thr Pro Pro Arg Arg

Ala Pro Ser Pro Asp Gly Phe Ser Pro Tyr Ser Pro Glu Glu Thr Ser
Arg Arg Val Asn Lys Val Met Arg Ala Arg Leu Tyr Leu Leu Gln Gln
Ile Gly Pro Asn Ser Phe Leu Ile Gly Gly Asp Ser Pro Asp Asn Lys
Tyr Arg Val Phe Ile Gly Pro Gln Asn Cys Ser Cys Gly Arg Gly Ala
Phe Cys Ile His Leu Leu Phe Val Met Leu Arg Val Phe Gln Leu Glu
Pro Ser Asp Pro Met Leu Trp Arg Lys Thr Leu Lys Asn Phe Glu Val
Glu Ser Leu Phe Gln Lys Tyr His Ser Arg Arg Ser Ser Arg Ile Lys
Ala Pro Ser Arg Asn Thr Ile Gln Lys Phe Val Ser Arg Met Ser Asn
Ser His Thr Leu Ser Ser Ser Ser Thr Ser Thr Ser Ser Ser Glu Asn
Ser Ile Lys Asp Glu Glu Glu Gln Met Cys Pro Ile Cys Leu Leu Gly
Met Leu Asp Glu Glu Ser Leu Thr Val Cys Glu Asp Gly Cys Arg Asn
Lys Leu His His His Cys Met Ser Ile Trp Ala Glu Glu Cys Arg Arg
Asn Arg Glu Pro Leu Ile Cys Pro Leu Cys Arg Ser Lys Trp Arg Ser
His Asp Phe Tyr Ser His Glu Leu Ser Ser Pro Val Glu Ser Pro Ala
Ser Leu Arg Ala Val Gln Gln Pro Ser Ser Pro Gln Gln Pro Val Ala
Gly Ser Gln Arg Arg Asn Gln Glu Ser Ser Phe Asn Leu Thr His Phe
Gly Thr Gln Gln Ile Pro Ser Ala Tyr Lys Asp Leu Ala Glu Pro Trp
Ile Gln Val Phe Gly Met Glu Leu Val Gly Cys Leu Phe Ser Arg Asn
Trp Asn Val Arg Glu Met Ala Leu Arg Arg Leu Ser His Asp Val Ser
Gly Ala Leu Leu Leu Ala Asn Gly Glu Ser Thr Gly Asn Ser Gly Gly
Gly Ser Gly Gly Ser Leu Ser Ala Gly Ala Ala Ser Gly Ser Ser Gln
Pro Ser Ile Ser Gly Asp Val Val Glu Ala Cys Cys Ser Val Leu Ser
Ile Val Cys Ala Asp Pro Val Tyr Lys Val Tyr Val Ala Ala Leu Lys
Thr Leu Arg Ala Met Leu Val Tyr Thr Pro Cys His Ser Leu Ala Glu
Arg Ile Lys Leu Gln Arg Leu Leu Arg Pro Val Val Asp Thr Ile Leu
Val Lys Cys Ala Asp Ala Asn Ser Arg Thr Ser Gln Leu Ser Ile Ser
Thr Val Leu Glu Leu Cys Lys Gly Gln Ala Gly Glu Leu Ala Val Gly
Arg Glu Ile Leu Lys Ala Gly Ser Ile Gly Val Gly Gly Val Asp Tyr
Val Leu Ser Cys Ile Leu Gly Asn Gln Ala Glu Ser Asn Asn Trp Gln
Glu Leu Leu Gly Arg Leu Cys Leu Ile Asp Arg Leu Leu Leu Glu Phe
Pro Ala Glu Phe Tyr Pro His Ile Val Ser Thr Asp Val Ser Gln Ala
Glu Pro Val Glu Ile Arg Tyr Lys Lys Leu Leu Ser Leu Leu Thr Phe

Ala Leu Gln Ser Ile Asp Asn Ser His Ser Met Val Gly Lys Leu Ser
Arg Arg Ile Tyr Leu Ser Ser Ala Arg Met Val Thr Ala Val Pro Ala
Val Phe Ser Lys Leu Val Thr Met Leu Asn Ala Ser Gly Ser Thr His
Phe Thr Arg Met Arg Arg Arg Leu Met Ala Ile Ala Asp Glu Val Glu
Ile Ala Glu Val Ile Gln Leu Gly Val Glu Asp Thr Val Asp Gly His
Gln Asp Ser Leu Gln Ala Val Ala Pro Thr Ser Cys Leu Glu Asn Ser
Ser Leu Glu His Thr Val His Arg Glu Lys Thr Gly Lys Gly Leu Ser
Ala Thr Arg Leu Ser Ala Ser Ser Glu Asp Ile Ser Asp Arg Leu Ala
Gly Val Ser Val Gly Leu Pro Ser Ser Thr Thr Thr Glu Gln Pro Lys
Pro Ala Val Gln Thr Lys Gly Arg Pro His Ser Gln Cys Leu Asn Ser
Ser Pro Leu Ser His Ala Gln Leu Met Phe Pro Ala Pro Ser Ala Pro
Cys Ser Ser Ala Pro Ser Val Pro Asp Ile Ser Lys His Arg Pro Gln
Ala Phe Val Pro Cys Lys Ile Pro Ser Ala Ser Pro Gln Thr Gln Arg
Lys Phe Ser Leu Gln Phe Gln Arg Asn Cys Ser Glu His Arg Asp Ser
Asp Gln Leu Ser Pro Val Phe Thr Gln Ser Arg Pro Pro Pro Ser Ser
Asn Ile His Arg Pro Lys Pro Ser Arg Pro Val Pro Gly Ser Thr Ser
Lys Leu Gly Asp Ala Thr Lys Ser Ser Met Thr Leu Asp Leu Gly Ser
Ala Ser Arg Cys Asp Asp Ser Phe Gly Gly Gly Gly Asn Ser Gly Asn
Ala Val Ile Pro Ser Asp Glu Thr Val Phe Thr Pro Val Glu Asp Lys
Cys Arg Leu Asp Val Asn Thr Glu Leu Asn Ser Ser Ile Glu Asp Leu
Leu Glu Ala Ser Met Pro Ser Ser Asp Thr Thr Val Thr Phe Lys Ser
Glu Val Ala Val Leu Ser Pro Glu Lys Ala Glu Asn Asp Asp Thr Tyr
Lys Asp Asp Val Asn His Asn Gln Lys Cys Lys Glu Lys Met Glu Ala
Glu Glu Glu Glu Ala Leu Ala Ile Ala Met Ala Met Ser Ala Ser Gln
Asp Ala Leu Pro Ile Val Pro Gln Leu Gln Val Glu Asn Gly Glu Asp
Ile Ile Ile Ile Gln Gln Asp Thr Pro Glu Thr Leu Pro Gly His Thr
Lys Ala Lys Gln Pro Tyr Arg Glu Asp Ala Glu Trp Leu Lys Gly Gln
Gln Ile Gly Leu Gly Ala Phe Ser Ser Cys Tyr Gln Ala Gln Asp Val
Gly Thr Gly Thr Leu Met Ala Val Lys Gln Val Thr Tyr Val Arg Asn
Thr Ser Ser Glu Gln Glu Glu Val Val Glu Ala Leu Arg Glu Glu Ile
Arg Met Met Gly His Leu Asn His Pro Asn Ile Ile Arg Met Leu Gly
Ala Thr Cys Glu Lys Ser Asn Tyr Asn Leu Phe Ile Glu Trp Met Ala

Gly Gly Ser Val Ala His Leu Leu Ser Lys Tyr Gly Ala Phe Lys Glu
Ser Val Val Ile Asn Tyr Thr Glu Gln Leu Leu Arg Gly Leu Ser Tyr
Leu His Glu Asn Gln Ile Ile His Arg Asp Val Lys Gly Ala Asn Leu
Leu Ile Asp Ser Thr Gly Gln Arg Leu Arg Ile Ala Asp Phe Gly Ala
Ala Ala Arg Leu Ala Ser Lys Gly Thr Gly Ala Gly Glu Phe Gln Gly
Gln Leu Leu Gly Thr Ile Ala Phe Met Ala Pro Glu Val Leu Arg Gly
Gln Gln Tyr Gly Arg Ser Cys Asp Val Trp Ser Val Gly Cys Ala Ile
Ile Glu Met Ala Cys Ala Lys Pro Pro Trp Asn Ala Glu Lys His Ser
Asn His Leu Ala Leu Ile Phe Lys Ile Ala Ser Ala Thr Thr Ala Pro
Ser Ile Pro Ser His Leu Ser Pro Gly Leu Arg Asp Val Ala Val Arg
Cys Leu Glu Leu Gln Pro Gln Asp Arg Pro Pro Ser Arg Glu Leu Leu
Lys His Pro Val Phe Arg Thr Thr Trp

mouse MEKK1 protein sequence

human MEKK1 protein sequence

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal

Asp Glu Val Glu
1

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 4 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal

Asp Thr Val Asp
1

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(v) FRAGMENT TYPE: internal

Asp Arg Pro Pro Ser Arg Glu Leu Leu Lys His Pro Val Glu Arg
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: peptide

- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Pro Pro Pro Ser Ser
1 5

SEQ ID NO: 10

Tyr Val Ala Asp

SEQ ID NO: 11

Asp Glu Val Asp

SEQ ID NO: 12

Met Gly Tyr Pro Tyr Asp Val Asp Tyr Ala Ser

SEQ ID NO: 13

Mouse MEKK1 full length cDNA sequence